

Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims

Claims 1-70 (Previously Canceled).

Claim 71. (Currently Amended) A recombinant double-stranded DNA molecule comprising ~~the following constituents~~:

- (i) a promoter functional in plants; and
- (ii) a DNA sequence ~~coding for~~ encoding a citrate synthase,

wherein said DNA sequence is fused to said promoter in antisense orientation so that the non-coding strand of said DNA sequence is transcribed[.]; and

wherein said DNA sequence exhibits sufficient sequence identity to an endogenous citrate synthase gene to reduce expression of said endogenous citrate synthase gene in a transgenic plant cell containing and transcribing the DNA molecule, as compared to the expression of said endogenous citrate synthase gene in a wild type plant cell, whereby said reduced citrate synthase expression leads to inhibition of flower formation, reduced sprouting of a tuber and/or improved storage capability of a storage organ in a plant comprising said transgenic plant cell or a plurality of said transgenic plant cells or a plurality of said transgenic plant cells as compared to a wild type plant.

Claims 72-73 (Previously Canceled).

Claim 74. (Currently Amended) The DNA molecule according to claim 71, wherein said DNA sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, a DNA sequence encoding the amino acid sequence of SEQ ID NO: 2, a DNA sequence encoding the amino acid sequence of SEQ ID NO: 4, a DNA sequence encoding the amino acid sequence of SEQ ID NO: 6, a DNA sequence that has at least ~~65~~ 80% sequence identity with the nucleotide sequence of SEQ ID NO: 1, a DNA sequence that has at least ~~65~~ 80% sequence identity with the nucleotide sequence of SEQ ID NO: 3, a DNA sequence that has at least ~~65~~ 80% sequence identity with the nucleotide sequence of SEQ ID NO: 5, a nucleotide sequence that encodes an amino acid sequence that has at least ~~65~~ 80% sequence identity with the amino acid sequence of SEQ ID NO: 2, a nucleotide sequence that encodes an amino acid sequence that has at least ~~65~~ 80% sequence identity with the amino acid sequence of SEQ ID NO: 4, and a nucleotide sequence that encodes an amino acid sequence that has at least ~~65~~ 80% sequence identity with the amino acid sequence of SEQ ID NO: 6;

~~wherein said DNA sequence exhibits sufficient sequence identity to an endogenous citrate synthase gene to reduce expression of said endogenous citrate synthase gene, relative to the expression of said endogenous citrate synthase gene in a wild type plant cell, when the DNA molecule is introduced and transcribed in a transgenic plant cell.~~

Claim 75. (Previously Presented) A vector comprising the DNA molecule according to claim 74.

Claim 76. (Previously Presented) A vector comprising the DNA molecule according to claim 71.

Claim 77. (Currently Amended) ~~The vector according to claim 76,~~
~~wherein said vector is~~ A plasmid pKS-CSa, deposited as DSM 8880.

Claim 78. (Currently Amended) ~~The vector according to claim 76,~~
~~wherein said vector is~~ A plasmid TCSAS, deposited as DSM 9359.

Claim 79. (Currently Amended) A recombinant double-stranded DNA molecule comprising ~~the following constituents:~~

- (i) a promoter functional in plants; and
- (ii) a portion of a DNA sequence ~~coding for~~ encoding a citrate synthase,

wherein said portion of said DNA sequence is at least 15 base pairs in length and is fused to said promoter in antisense orientation so that the non-coding strand of said DNA sequence is transcribed; and

wherein said DNA sequence is of sufficient length to reduce expression of an endogenous citrate synthase gene, ~~relative~~ in a transgenic plant cell containing and transcribing the DNA molecule, as compared to the expression of said

endogenous citrate synthase gene in a wild type plant cell, ~~when the DNA molecule is introduced and transcribed in a transgenic plant cell~~ whereby said reduced citrate synthase expression leads to inhibition of flower formation, reduced sprouting of a tuber and/or improved storage capability of a storage organ in a plant comprising said transgenic plant cell or a plurality of said transgenic cells as compared to a wild type plant.

Claim 80. (Currently Amended) A vector comprising the DNA molecule according to claim 79 or 121.

Claim 81. (Currently Amended) A bacterial cell comprising:

- (a) the DNA molecule according to any one of claims 71, 74, ~~or 79 or 121~~, or
- (b) ~~the a vector according to any one of claims 75-78 or 80~~ comprising said DNA molecule.

Claim 82. (Currently Amended) A transgenic plant cell comprising:

- (a) the DNA molecule according to ~~either claim~~ any one of claims 71, 74, or 79 or 121, or
- (b) ~~the a vector according to any one of claims 75-78 or 80~~ comprising said DNA molecule.

Claim 83. (Previously Presented) A transgenic plant comprising the transgenic plant cell according to claim 82, wherein said transgenic plant cell has a reduced citrate synthase activity in comparison to the citrate synthase activity of a wild type plant cell.

Claims 84-99 (Previously Canceled).

Claim 100. (Currently Amended) A transgenic plant comprising transgenic plant cells having integrated into their genome a recombinant double stranded DNA molecule comprising:

(a) a promoter functional in plant cells; and

(b) a DNA sequence ~~coding for~~ encoding a citrate synthase or a part of said DNA sequence of at least 15 base pairs, wherein said DNA sequence or said part thereof is operably linked to said promoter;

wherein transcription of said DNA molecule suppresses an endogenous citrate synthase activity in said transgenic plant such that said transgenic plant cells have a reduced citrate synthase activity in comparison to the citrate synthase activity of wild type plant cells; and

wherein said transgenic plant, in comparison to a wild type plant, displays an inhibition of flower formation, a reduction of sprouting of a tuber and/or an increase in storage capability of a storage organ.

Claim 101. (Previously Presented) The transgenic plant according to claim 100, which is selected from the group consisting of a grain plant, a fruit plant, a vegetable plant, an ornamental plant, a plant that develops tubers or beet as a storage organ, tobacco, potato, manioc, rapeseed and sugar cane.

Claim 102. (Previously Presented) A storage organ of a plant according to any one of claims 100 or 101 comprising said transgenic plant cells having a reduced citrate synthase activity in comparison to the citrate synthase activity of wild type plant cells.

Claim 103. (Previously Presented) The storage organ according to claim 102 which is a tuber.

Claim 104. (Currently Amended) ~~The~~ A transgenic plant ~~according to~~ claim 100, comprising a recombinant DNA comprising the following constituents comprising transgenic plant cells having integrated into their genome a recombinant double stranded DNA molecule comprising:

- a) a promoter functional in plants; and
- b) a DNA sequence ~~coding for~~ encoding a citrate synthase;

wherein said DNA sequence is fused to said promoter in antisense orientation so that the non-coding strand of said DNA sequence is transcribed, and wherein said DNA sequence exhibits sufficient sequence identity to an endogenous citrate synthase gene to reduce expression of said endogenous citrate

synthase gene in said transgenic plant cell, as compared to the expression of said endogenous citrate synthase gene in a wild type plant cell, and
wherein said transgenic plant, in comparison to a wild type plant,
displays an inhibition of flower formation, a reduction of sprouting of a tuber and/or
an increase in storage capability of a storage organ.

Claim 105. (Currently Amended) The transgenic plant according to claim 104, wherein said citrate synthase ~~comprises the amino acid sequence of SEQ ID NO: 2 or an amino acid sequence having a sequence identity of at least 65% to the sequence of SEQ ID NO: 2~~ comprises an amino acid sequence selected from the group consisting of: the amino acid sequence of SEQ ID NO:2, an amino acid sequence having a sequence identity of at least 80% to the sequence of SEQ ID NO:2, the amino acid sequences of SEQ ID NO:4, an amino acid sequence having a sequence identity of at least 80% to the sequence of SEQ ID NO:4, the amino acids of SEQ ID NO:6, and a amino acid sequence having a sequence identity of at least 80% to the sequence of SEQ ID NO:6.

Claim 106. (Currently Amended) The transgenic plant according to claim 104, wherein said citrate synthase comprises the amino acid sequence of SEQ ID NO: 4 or an amino acid sequence having a sequence identity of at least ~~65~~ 80% to the sequence of SEQ ID NO: 4.

Claim 107. (Currently Amended) The transgenic plant according to claim 104, wherein said citrate synthase comprises the amino acid sequence of SEQ ID NO: 6 or an amino acid sequence having a sequence identity of at least ~~65~~ 80% to the sequence of SEQ ID NO: 6.

Claim 108. (Currently Amended) The transgenic plant ~~of~~ according to claim 104, wherein said DNA sequence comprises the nucleotide sequence of SEQ ID ~~No: NO:~~ 1 or a nucleotide sequence having at least ~~65~~ 80% sequence identity to the sequence of SEQ ID NO: 1.

Claim 109. (Currently Amended) The transgenic plant ~~of~~ according to claim 104, wherein said DNA sequence comprises the nucleotide sequence of SEQ ID ~~No: NO:~~ 3 or a nucleotide sequence having at least ~~65~~ 80% sequence identity to the sequence of SEQ ID NO: 3.

Claim 110. (Amended) The transgenic plant ~~of~~ according to claim 104, wherein said DNA sequence comprises the nucleotide sequence of SEQ ID ~~No: NO:~~ 5 or a nucleotide sequence having at least ~~65~~ 80% sequence identity to the sequence of SEQ ID NO: 5.

Claim 111. (Previously Presented) A seed of the transgenic plant according to any one of claims 100, 101 or 104–110.

Claim 112. (Currently Amended) A process for inhibiting flower formation in a transgenic plant compared to flower formation in a wild type plant, wherein the citrate synthase activity in the cells of said transgenic plant are reduced compared to the citrate synthase activity in wild type plant cells, comprising the steps of:

(a) introducing into a plant cell a recombinant double-stranded DNA molecule to generate a transgenic plant cell, said DNA molecule comprising

(i) a promoter functional in plant cells; and

(ii) a DNA sequence ~~coding for~~ encoding a citrate synthase or a part of said DNA sequence, which is at least 15 bp and is sufficient in length to suppress endogenous citrate synthase activity,

wherein said DNA sequence is operably linked to said promoter

and wherein said DNA molecule forms transcripts through which an endogenous citrate synthase activity can be suppressed; and

(b) regenerating the transgenic plant from said transgenic cell, wherein the reduced citrate synthase activity of said transgenic plant inhibits flower formation as compared to flower formation in a wild type plant.

Claim 113. (Currently Amended) A process to increase the storage capability of a storage organs organ in a transgenic plant compared to the storage capability of a storage organs organ in a wild type plant, wherein the citrate synthase activity in the cells of said transgenic plant are reduced compared to the citrate synthase activity in wild type plant cells, comprising the steps of:

(a) introducing into a plant cell a recombinant double-stranded DNA molecule to generate a transgenic plant cell, said DNA molecule comprising

(i) a promoter functional in plant cells; and

(ii) a DNA sequence ~~coding for~~ encoding a citrate synthase or a part of said DNA sequence, which is at least 15 bp and is sufficient in length to suppress endogenous citrate synthase activity,

wherein said DNA sequence is operably linked to said promoter and

wherein said DNA molecule forms transcripts through which an endogenous citrate synthase activity can be suppressed; and

(b) regenerating the transgenic plant from said transgenic cell, wherein the reduced citrate synthase activity of said transgenic plant improves storage capability of a storage organ as compared to storage capability of a storage organ in a wild type plant.

Claim 114. (Currently Amended) A process for reducing the sprouting of ~~tubers~~ a tuber of a transgenic tuberous plant compared to the sprouting of ~~tubers~~ a tuber in a wild type plant, wherein the citrate synthase activity in the cells of said transgenic plant are reduced compared to the citrate synthase activity in wild type plant cells, comprising the steps of:

(a) introducing into a plant cell a recombinant double-stranded DNA molecule to generate a transgenic plant cell, said DNA molecule comprising

(i) a promoter functional in plant cells; and

(ii) a DNA sequence ~~coding for~~ encoding a citrate synthase or a part of said DNA sequence, which is at least 15 bp and is sufficient in length to suppress endogenous citrate synthase activity,

wherein said DNA sequence is operably linked to said promoter and

wherein said DNA molecule forms transcripts through which an endogenous citrate synthase activity can be suppressed; and

(b) regenerating the transgenic plant from said transgenic cell, wherein the reduced citrate synthase activity of said transgenic plant reduces sprouting of a tuber as compared to sprouting of a tuber in a wild type plant.

Claim 115. (Previously Presented) The process according to any one of claims 112 to 114, wherein antisense RNA is transcribed from said DNA sequence.

Claim 116. (Currently Amended) The process according to claim 115, wherein said DNA sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, a DNA sequence that has at least ~~65~~ 80% sequence identity with the nucleotide sequence of SEQ ID NO: 1, a DNA sequence that has at least ~~65~~ 80% sequence identity with the nucleotide sequence of SEQ ID NO: 3, and a DNA sequence that has at least ~~65~~ 80% sequence identity with the nucleotide sequence of SEQ ID NO: 5,

wherein said DNA sequence exhibits sufficient sequence identity to an endogenous citrate synthase gene to reduce expression of said endogenous citrate

synthase gene ~~when the DNA molecule is introduced and transcribed in a transgenic plant cell~~ in a plant cell containing and transcribing the DNA molecule.

Claim 117. (Currently Amended) The process according to claim 115, wherein said DNA sequence codes for an amino acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, an amino acid sequence that has at least ~~65~~ 80% sequence identity with the amino acid sequence of SEQ ID NO: 2, an amino acid sequence that has at least ~~65~~ 80% sequence identity with the amino acid sequence of SEQ ID NO: 4, and an amino acid sequence that has at least ~~65~~ 80% sequence identity with the amino acid sequence of SEQ ID NO: 6;

wherein said DNA sequence exhibits sufficient sequence identity to an endogenous citrate synthase gene to reduce expression of said endogenous citrate synthase gene ~~when the DNA molecule is introduced and transcribed in a transgenic plant cell~~ in a plant cell containing and transcribing the DNA molecule.

Claim 118. (Currently Amended) A transgenic plant comprising the recombinant double-stranded DNA molecule according to ~~claim~~ any one of claims 71, 74, 79 or 121-123, integrated into the genome of plant cells of said transgenic plant.

Claim 119. (Previously Presented) A seed of the transgenic plant according to claim 118.

Claim 120. (Previously Presented) A seed of the transgenic plant according to claim 83.

Claim 121. (New) The DNA molecule according to claim 79, wherein said DNA sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, a DNA sequence encoding the amino acid sequence of SEQ ID NO: 2, a DNA sequence encoding the amino acid sequence of SEQ ID NO: 4, a DNA sequence encoding the amino acid sequence of SEQ ID NO: 6, a DNA sequence that has at least 80% sequence identity with the nucleotide sequence of SEQ ID NO: 1, a DNA sequence that has at least 80% sequence identity with the nucleotide sequence of SEQ ID NO: 3, a DNA sequence that has at least 80% sequence identity with the nucleotide sequence of SEQ ID NO: 5, a nucleotide sequence that encodes an amino acid sequence that has at least 80% sequence identity with the amino acid sequence of SEQ ID NO: 2, a nucleotide sequence that encodes an amino acid sequence that has at least 80% sequence identity with the amino acid sequence of SEQ ID NO: 4, and a nucleotide sequence that encodes an amino acid sequence that has at least 80% sequence identity with the amino acid sequence of SEQ ID NO: 6.

Claim 122. (New) The DNA molecule according to claim 71, wherein the DNA sequence is from a plant of the *Solanaceae* family or the *Chenopodiaceae* family.

Claim 123. (New) The DNA molecule according to claim 79, wherein the DNA sequence is from a plant of the *Solanaceae* family or the *Chenopodiaceae* family.

Claim 124. (New) A method for reducing the synthesis of an endogenous citrate synthase in a plant cell compared to the synthesis of a citrate synthase in a wild type plant cell, comprising introducing into the plant cell the vector according to any one of claims 75, 76 or 80 to obtain a transgenic plant cell and transcribing from said DNA molecule non-translatable mRNA, wherein said transcribing results in a reduction in the synthesis of endogenous citrate synthase in the transgenic plant cell as compared to said wild type plant cell.

Claim 125. (New) The transgenic plant according to claim 83 selected from the group consisting of a grain plant, a fruit plant, a vegetable plant, an ornamental plant, a plant that develops tubers or beet as a storage organ, tobacco, potato, manioc, rapeseed and sugar cane.

Claim 126. (New) A storage organ of a plant according to claim 83 comprising said transgenic plant cells having a reduced citrate synthase activity as compared to the citrate synthase activity of wild type plant cells.